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Susumu, ITO

<120> TITLE OF INVENTION: GENE ENCODING ALKALINE LIQUEFYING ALPHA-AMYLASE

<130> FILE REFERENCE: 2173-106P

<140> CURRENT APPLICATION NUMBER:10829331

<141> CURRENT FILING DATE:2004-04-22

<150> PRIOR APPLICATION NUMBER: US/08/952,741

<151> PRIOR FILING DATE: 1997-11-25

<160> NUMBER OF SEQ ID NOS: 11

<170> SOFTWARE: PatentIn Ver. 2.0

<210> SEQ ID NO 1

<211> LENGTH: 1776

<212> TYPE: DNA

<213> ORGANISM: Bacillus sp.

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (145)..(1692)

<400> SEQUENCE: 1

atataaattt gaaatgaaca cctatgaaaa tatggtagcg attgcgcgac gagaaaaaac
60

ttgggagtta ggaagtgata ttaaaggatt ttttttgact tgttgtgaaa acgcttgcac
120

aaattgaagg agagggtgct tttt atg aaa ctt cat aac cgt ata att agc
171

Met Lys Leu His Asn Arg Ile Ile Ser
1 5
gta cta tta aca cta ttg tta gct gta gct gtt ttg ttt cca tat atg
219

Val Leu Leu Thr Leu Leu Leu Ala Val Ala Val Leu Phe Pro Tyr Met
10 15 20 25
acg gaa cca gca caa gcc cat cat aat ggg acg aat ggg acc atg atg
267

Thr Glu Pro Ala Gln Ala His His Asn Gly Thr Asn Gly Thr Met Met
30 35 40
cag tat ttt gaa tgg cat ttg cca aat gac ggg aac cac tgg aac agg
315

Gln Tyr Phe Glu Trp His Leu Pro Asn Asp Gly Asn His Trp Asn Arg
45 50 55
tta cga gat gac gca gct aac tta aag agt aaa ggg att acc gct gtt
363

Leu Arg Asp Asp Ala Ala Asn Leu Lys Ser Lys Gly Ile Thr Ala Val
60 65 70
tgg att cct cct gca tgg aag ggg act tcg caa aat gat gtt ggg tat
411

Trp Ile Pro Pro Ala Trp Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr
75 80 85
ggg gcc tat gat ttg tac gat ctt ggt gag ttt aac caa aag gga acc
459

Gly Ala Tyr Asp Leu Tyr Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr
90 95 100 105
gtc cgt aca aaa tat ggc aca agg agt cag ttg caa ggt gcc gtg aca
507

Val Arg Thr Lys Tyr Gly Thr Arg Ser Gln Leu Gln Gly Ala Val Thr
110 115 120

555	tct ttg aaa aat aac ggg att caa gtt tat ggg gat gtc gtg atg aat
	Ser Leu Lys Asn Asn Gly Ile Gln Val Tyr Gly Asp Val Val Met Asn
	125 130 135
603	cat aaa ggt gga gca gac ggg aca gag atg gta aat gcg gtg gaa gtg
	His Lys Gly Gly Ala Asp Gly Thr Glu Met Val Asn Ala Val Glu Val
	140 145 150
651	aac cga agc aac cga aac caa gaa ata tca ggt gaa tac acc att gaa
	Asn Arg Ser Asn Arg Asn Gln Glu Ile Ser Gly Glu Tyr Thr Ile Glu
	155 160 165
699	gca tgg acg aaa ttt gat ttc cct gga aga gga aat acc cat tcc aac
	Ala Trp Thr Lys Phe Asp Phe Pro Gly Arg Gly Asn Thr His Ser Asn
	170 175 180 185
747	ttt aaa tgg cgc tgg tat cat ttt gat ggg aca gat tgg gat cag tca
	Phe Lys Trp Arg Trp Tyr His Phe Asp Gly Thr Asp Trp Asp Gln Ser
	190 195 200
795	cgt cag ctt cag aac aaa ata tat aaa ttc aga ggt acc gga aag gca
	Arg Gln Leu Gln Asn Lys Ile Tyr Lys Phe Arg Gly Thr Gly Lys Ala
	205 210 215
843	tgg gac tgg gaa gta gat ata gag aac ggc aac tat gat tac ctt atg
	Trp Asp Trp Glu Val Asp Ile Glu Asn Gly Asn Tyr Asp Tyr Leu Met
	220 225 230
891	tat gca gac att gat atg gat cat cca gaa gta atc aat gaa ctt aga
	Tyr Ala Asp Ile Asp Met Asp His Pro Glu Val Ile Asn Glu Leu Arg
	235 240 245
939	aat tgg gga gtt tgg tat aca aat aca ctt aat cta gat gga ttt aga
	Asn Trp Gly Val Trp Tyr Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg
	250 255 260 265
987	atc gat gct gtg aaa cat att aaa tac agc tat acg aga gat tgg cta
	Ile Asp Ala Val Lys His Ile Lys Tyr Ser Tyr Thr Arg Asp Trp Leu
	270 275 280
1035	aca cat gtg cgt aac acc aca ggt aaa cca atg ttt gca gtt gca gaa
	Thr His Val Arg Asn Thr Thr Gly Lys Pro Met Phe Ala Val Ala Glu
	285 290 295
1083	ttt tgg aaa aat gac ctt gct gca atc gaa aac tat tta aat aaa aca
	Phe Trp Lys Asn Asp Leu Ala Ala Ile Glu Asn Tyr Leu Asn Lys Thr
	300 305 310
1131	agt tgg aat cac tcc gtg ttc gat gtt cct ctt cat tat aat ttg tac
	Ser Trp Asn His Ser Val Phe Asp Val Pro Leu His Tyr Asn Leu Tyr
	315 320 325
1179	aat gca tct aat agt ggt ggc tat ttt gat atg aga aat att tta aat
	Asn Ala Ser Asn Ser Gly Gly Tyr Phe Asp Met Arg Asn Ile Leu Asn
	330 335 340 345
1227	ggg tct gtc gta caa aaa cac cct ata cat gca gtc aca ttt gtt gat
	Gly Ser Val Val Gln Lys His Pro Ile His Ala Val Thr Phe Val Asp
	350 355 360
	aac cat gac tct cag cca gga gaa gca ttg gaa tcc ttt gtt caa tcg

1275 Asn His Asp Ser Gln Pro Gly Glu Ala Leu Glu Ser Phe Val Gln Ser
365 370 375
tgg ttc aaa cca ctg gca tat gca ttg att ctg aca agg gag caa ggt

1323 Trp Phe Lys Pro Leu Ala Tyr Ala Leu Ile Leu Thr Arg Glu Gln Gly
380 385 390
tac cct tcc gta ttt tac ggt gat tac tac ggt ata cca act cat ggt

1371 Tyr Pro Ser Val Phe Tyr Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly
395 400 405
gtt cct tcg atg aaa tct aaa att gat cca ctt ctg cag gca cgt caa

1419 Val Pro Ser Met Lys Ser Lys Ile Asp Pro Leu Leu Gln Ala Arg Gln
410 415 420 425
acg tat gcc tac gga acc caa cat gat tat ttt gat cat cat gat att

1467 Thr Tyr Ala Tyr Gly Thr Gln His Asp Tyr Phe Asp His His Asp Ile
430 435 440
atc ggc tgg acg aga gaa ggg gac agc tcc cac cca aat tca gga ctt

1515 Ile Gly Trp Thr Arg Glu Gly Asp Ser Ser His Pro Asn Ser Gly Leu
445 450 455
gca act att atg tcc gat ggg cca ggg ggt aat aaa tgg atg tat gtc

1563 Ala Thr Ile Met Ser Asp Gly Pro Gly Gly Asn Lys Trp Met Tyr Val
460 465 470
ggg aaa cat aaa gct ggc caa gta tgg aga gat atc acc gga aat agg

1611 Gly Lys His Lys Ala Gly Gln Val Trp Arg Asp Ile Thr Gly Asn Arg
475 480 485
tct ggt acc gtc acc att aat gca gat ggt tgg ggg aat ttc act gta

1659 Ser Gly Thr Val Thr Ile Asn Ala Asp Gly Trp Gly Asn Phe Thr Val
490 495 500 505
aac gga ggg gca gtt tcg gtt tgg gtg aag caa taaataagga acaagaggcg

1712 Asn Gly Gly Ala Val Ser Val Trp Val Lys Gln
510 515
aaaattactt tcctacatgc agagctttcc gatcactcat acaccaata taaattggaa

1772 gctt

1776

<210> SEQ ID NO 2

<211> LENGTH: 516

<212> TYPE: PRT

<213> ORGANISM: Bacillus sp.

<400> SEQUENCE: 2

Met Lys Leu His Asn Arg Ile Ile Ser Val Leu Leu Thr Leu Leu Leu
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Ala Val Ala Val Leu Phe Pro Tyr Met Thr Glu Pro Ala Gln Ala His
20 25 30
His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp His Leu
35 40 45
Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ala Asn
50 55 60
Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp Lys
65 70 75 80
Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp
85 90 95

Leu	Gly	Glu	Phe	Asn	Gln	Lys	Gly	Thr	Val	Arg	Thr	Lys	Tyr	Gly	Thr	
			100					105					110			
Arg	Ser	Gln	Leu	Gln	Gly	Ala	Val	Thr	Ser	Leu	Lys	Asn	Asn	Gly	Ile	
		115					120					125				
Gln	Val	Tyr	Gly	Asp	Val	Val	Met	Asn	His	Lys	Gly	Gly	Ala	Asp	Gly	
	130					135					140					
Thr	Glu	Met	Val	Asn	Ala	Val	Glu	Val	Asn	Arg	Ser	Asn	Arg	Asn	Gln	
145					150					155					160	
Glu	Ile	Ser	Gly	Glu	Tyr	Thr	Ile	Glu	Ala	Trp	Thr	Lys	Phe	Asp	Phe	
			165						170					175		
Pro	Gly	Arg	Gly	Asn	Thr	His	Ser	Asn	Phe	Lys	Trp	Arg	Trp	Tyr	His	
			180					185					190			
Phe	Asp	Gly	Thr	Asp	Trp	Asp	Gln	Ser	Arg	Gln	Leu	Gln	Asn	Lys	Ile	
		195					200					205				
Tyr	Lys	Phe	Arg	Gly	Thr	Gly	Lys	Ala	Trp	Asp	Trp	Glu	Val	Asp	Ile	
	210					215					220					
Glu	Asn	Gly	Asn	Tyr	Asp	Tyr	Leu	Met	Tyr	Ala	Asp	Ile	Asp	Met	Asp	
225					230					235					240	
His	Pro	Glu	Val	Ile	Asn	Glu	Leu	Arg	Asn	Trp	Gly	Val	Trp	Tyr	Thr	
			245						250					255		
Asn	Thr	Leu	Asn	Leu	Asp	Gly	Phe	Arg	Ile	Asp	Ala	Val	Lys	His	Ile	
			260					265					270			
Lys	Tyr	Ser	Tyr	Thr	Arg	Asp	Trp	Leu	Thr	His	Val	Arg	Asn	Thr	Thr	
		275					280					285				
Gly	Lys	Pro	Met	Phe	Ala	Val	Ala	Glu	Phe	Trp	Lys	Asn	Asp	Leu	Ala	
	290					295					300					
Ala	Ile	Glu	Asn	Tyr	Leu	Asn	Lys	Thr	Ser	Trp	Asn	His	Ser	Val	Phe	
305					310					315					320	
Asp	Val	Pro	Leu	His	Tyr	Asn	Leu	Tyr	Asn	Ala	Ser	Asn	Ser	Gly	Gly	
			325						330					335		
Tyr	Phe	Asp	Met	Arg	Asn	Ile	Leu	Asn	Gly	Ser	Val	Val	Gln	Lys	His	
		340						345					350			
Pro	Ile	His	Ala	Val	Thr	Phe	Val	Asp	Asn	His	Asp	Ser	Gln	Pro	Gly	
		355					360					365				
Glu	Ala	Leu	Glu	Ser	Phe	Val	Gln	Ser	Trp	Phe	Lys	Pro	Leu	Ala	Tyr	
	370					375					380					
Ala	Leu	Ile	Leu	Thr	Arg	Glu	Gln	Gly	Tyr	Pro	Ser	Val	Phe	Tyr	Gly	
385					390					395					400	
Asp	Tyr	Tyr	Gly	Ile	Pro	Thr	His	Gly	Val	Pro	Ser	Met	Lys	Ser	Lys	
			405						410				415			
Ile	Asp	Pro	Leu	Leu	Gln	Ala	Arg	Gln	Thr	Tyr	Ala	Tyr	Gly	Thr	Gln	
			420					425					430			
His	Asp	Tyr	Phe	Asp	His	His	Asp	Ile	Ile	Gly	Trp	Thr	Arg	Glu	Gly	
		435					440					445				
Asp	Ser	Ser	His	Pro	Asn	Ser	Gly	Leu	Ala	Thr	Ile	Met	Ser	Asp	Gly	
	450					455					460					
Pro	Gly	Gly	Asn	Lys	Trp	Met	Tyr	Val	Gly	Lys	His	Lys	Ala	Gly	Gln	
465					470					475					480	
Val	Trp	Arg	Asp	Ile	Thr	Gly	Asn	Arg	Ser	Gly	Thr	Val	Thr	Ile	Asn	
			485						490					495		
Ala	Asp	Gly	Trp	Gly	Asn	Phe	Thr	Val	Asn	Gly	Gly	Ala	Val	Ser	Val	
			500					505					510			
Trp	Val	Lys	Gln													
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<210> SEQ ID NO 3
 <211> LENGTH: 22
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: any n = a,c,t or g

<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence:Primer
<400> SEQUENCE: 3
tngaygcngt naarcayath aa
22

<210> SEQ ID NO 4
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: any n = a,c,t or g
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence:Primer
<400> SEQUENCE: 4
tcrtgrttrt cnacraangt nacngc
26

<210> SEQ ID NO 5
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence:Primer
<400> SEQUENCE: 5
agccaatctc tcgtatagct gta
23

<210> SEQ ID NO 6
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence:Primer
<400> SEQUENCE: 6
gtacaaaaac accctataca tg
22

<210> SEQ ID NO 7
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence:Primer
<400> SEQUENCE: 7
aatggwacwa tgatgcakta
20

<210> SEQ ID NO 8
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence:Primer
<400> SEQUENCE: 8
catttgcaa atgccattca aa
22

<210> SEQ ID NO 9
<211> LENGTH: 21
<212> TYPE: DNA